THE EMBODIMENTS OF THE INVENTION IN WHICH AN EXCLUSIVE PROPERTY OF PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. A method of detecting an epigenetic abnormality associated with a disease comprising, identifying, within a eukaryotic genome, a locus having a hypomethylated sequence specific for said disease and an endogenous multi-copy DNA element.

2. The method of claim 1, wherein said step of identifying comprises separate steps of identifying said disease-specific hypomethylated sequence and identifying said endogenous multi-copy DNA element.

3. The method of claim 2, wherein the steps may be performed in any order.

4. The method of claim 1, wherein said disease-specific hypomethylated sequence and said endogenous multi-copy DNA element are within 10 kilobases of separation.

5. The method of claim 1, wherein said endogenous multi-copy DNA element is a retroelement that is normally methylated.

6. The method of claim 5, wherein said retroelement is selected from the group consisting of endogenous retroviral sequences (ERV), SINE sequences, Alu sequences, LINE sequences, and L1 sequences.

7. A method of identifying a chromosomal region associated with a disease state comprising:
identifying a locus, within DNA obtained from said diseased sample, that has a DNA sequence that is hypomethylated and an endogenous multi-copy DNA element, wherein the DNA sequence is methylated in a non-disease sample and wherein the

chromosomal region consists of from about 1 to about 10 DNA coding sequences that are proximal to the identified locus.

8. A method of identifying a DNA coding sequence having an epigenetically altered expression pattern that contributes to a disease in an organism comprising:
identifying a locus, within DNA obtained from said diseased sample, that has a DNA sequence that is hypomethylated and an endogenous multi-copy DNA element, said DNA sequence being methylated in a non-disease sample; and
comparing expression patterns of the DNA coding sequence that comprises, or that is located proximal to, said identified locus within said diseased sample and said non-diseased sample, to identify said DNA coding sequence having an epigenetically altered expression pattern.

9. The method of claim 8, wherein said disease is selected from the group consisting of Huntingdon's disease, schizophrenia, and bipolar disorder.

10. A method of diagnosing an epigenetic abnormality correlated with a disease comprising:
identifying a DNA sequence that is hypomethylated within a locus that has an endogenous multi-copy DNA element and is obtained from a diseased sample, said DNA sequence being methylated in a non-disease sample.

11. Method of detecting an epigenetic abnormality associated with a non-Mendelian disease, said method comprising:

a) extraction of genomic DNA from a sample that exhibits characteristics of a non-Mendelian disease;

b) digestion of said genomic DNA with a methylation-sensitive restriction enzyme to produce a pool of restricted DNA fragments;

c) fractionation of said pool of restricted DNA fragments to obtain DNA fragments of a desired size;

d) amplification of at least a segment of said DNA fragments of a desired size with primers that anneal to an endogenous DNA element to produce a PCR product;

e) cloning of said PCR product into a sequencing vector;

f) sequence determination of said PCR product to obtain a sequence of said PCR product;

g) comparing said sequence against a genomic database to assign a locus for said epigenetic abnormality associated with a non-Mendelian disease.

12. The method of claim 11, wherein said non-Mendelian disease is selected from the group consisting of schizophrenia, bipolar disorder, cancer, and diabetes.

13. The method of claim 11, wherein said sample that exhibits characteristics of a non-Mendelian disease is brain tissue.

14. The method of claim 13, wherein said sample that exhibits characteristics of a non-Mendelian disease is selected from the group consisting of frontal cortex and prefrontal cortex.

15. The method of claim 11, wherein said desired size is less than 10 kb.

16. The method of claim 11, wherein said endogenous DNA element is a multi-copy DNA element.

17. The method of claim 16, wherein said multi-copy DNA element is selected from the group consisting of endogenous retroviral sequence, LINE, SINE, L1, and Alu.

18. The method of claim 11, wherein said methylation-sensitive restriction enzyme is selected from the group consisting of AatII (GACGTC); Bsh1236I (CGCG); Bsh1285I (CGRYCG); BshTI (ACCGGT); Bsp68I (TCGCGA); Bsp119I (TTCGAA); Bsp143II (RGCGCY); Bsu15I (ATCGAT); Cfr10I (RCCGGY); Cfr42I (CCGCGG); CpoI (CGGWCCG); Eco47III (AGCGCT); Eco52I (CGGCCG); Eco72I (CACGTG); Eco105I (TACGTA); EheI (GGCGCC); Esp3I (CGTCTC); FspAI

(RTGCGCAY); Hin1I (GRCGYC); Hin6I (GCGC); HpaII (CCGG); Kpn2I (TCCGGA); MluI (ACGCGT); NotI (GCGGCCGC); NsbI (TGCGCA); PauI (GCGCGC); PdiI (GCCGGC); Pfl23II (CGTACG); Psp1406I (AACGTT); PvuI (CGATCG); SalI (GTCGAC); SmaI (CCCGGG); SmuI (CCCGC); TaiI (ACGT); and TauI (GCSGC).

19. Method of identifying a gene having an epigenetically altered expression pattern that contributes to a non-Mendelian disease in an organism, said method comprising:

a) extraction of genomic DNA from a sample that exhibits characteristics of a non-Mendelian disease;

b) digestion of said genomic DNA with a methylation-sensitive restriction enzyme to produce a pool of restricted DNA fragments;

c) fractionation of said pool of restricted DNA fragments to obtain DNA fragments of a desired size;

d) amplification of at least a segment of said DNA fragments of a desired size with primers that anneal to an endogenous DNA element to produce a PCR product;

e) cloning of said PCR product into a sequencing vector;

f) sequence determination of said PCR product to obtain a sequence of said PCR product;

g) comparing said sequence against a genomic database to assign a locus for said epigenetic abnormality associated with a non-Mendelian disease;

h) searching said database to identify a gene located proximal to said locus;

i) comparing expression patterns of said gene located proximal to said locus within a test sample that exhibits characteristics of said non-Mendelian disease with expression patterns of a corresponding gene within a control sample to identify said gene having an epigenetically altered expression pattern.

20. A gene isolated by the method of claim 19.

21. Method of isolating a probe for detecting an epigenetic abnormality associated with a non-Mendelian disease, said method comprising:

a) extraction of genomic DNA from a sample that exhibits characteristics of a non-Mendelian disease;

b) digestion of said genomic DNA with a methylation-sensitive restriction enzyme to produce a pool of restricted DNA fragments;

c) fractionation of said pool of restricted DNA fragments to obtain DNA fragments of a desired size;

d) amplification of at least a segment of said DNA fragments of a desired size with primers that anneal to an endogenous DNA element to produce a PCR product;

e) using said PCR product as said probe to detect said epigenetic abnormality associated with a non-Mendelian disease in another sample.

22. A probe isolated by the method of claim 21.

23. A method of detecting a disease associated with an epigenetic abnormality comprising, identifying, within a eukaryotic genome, a locus having a hypomethylated sequence specific for said disease and an endogenous multi-copy DNA element.

24. A method of diagnosing a disease correlated with an epigenetic abnormality comprising:

identifying a DNA sequence that is hypomethylated within a locus that has an endogenous multi-copy DNA element and is obtained from a diseased sample, said DNA sequence being methylated in a non-disease sample.